

0590
2507

47



ENTERED

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/045,815

DATE: 05/02/2002 8.6

TIME: 15:43:53

Input Set : A:\06501-091001.TXT

Output Set: N:\CRF3\05022002\J045815.raw

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4 <110> APPLICANT: Wadhwa, Renu
5      Sugihara, Takashi
6      Ohide, Akiko
8 <120> TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
10 <130> FILE REFERENCE: 06501-091001
12 <140> CURRENT APPLICATION NUMBER: US 10/045,815
13 <141> CURRENT FILING DATE: 2001-10-26
15 <150> PRIOR APPLICATION NUMBER: PCT/JP00/02731
16 <151> PRIOR FILING DATE: 2000-04-26
18 <150> PRIOR APPLICATION NUMBER: JP 11/118806
19 <151> PRIOR FILING DATE: 1999-04-26
21 <160> NUMBER OF SEQ ID NOS: 15
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 2829
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (52)...(1140)
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35 ctccggcctt ggtggcgggt ggctggcgggt tccgttaggt ctgagggagc g atg gcg      57
36                                     Met Ala
37                                     1
39 gta cgc gcg ttg aag ctg ctg acc aca ctg ctg gct gtc gtg gcc gct      105
40 Val Arg Ala Leu Lys Leu Leu Thr Thr Leu Leu Ala Val Val Ala Ala
41      5      10      15
43 gcc tcc caa gcc gag gtc gag tcc gag gca gga tgg gcc atg gtg acg      153
44 Ala Ser Gln Ala Glu Val Glu Ser Glu Ala Gly Trp Gly Met Val Thr
45      20      25      30
47 cct gat ctg ctc ttc gcc gag ggg acc gca gcc tac gcg cgc ggg gac      201
48 Pro Asp Leu Leu Phe Ala Glu Gly Thr Ala Ala Tyr Ala Arg Gly Asp
49 35      40      45      50
51 tgg ccc ggg gtg gtc ctg agc atg gaa cgg gcg ctg cgc tcc cgg gca      249
52 Trp Pro Gly Val Val Leu Ser Met Glu Arg Ala Leu Arg Ser Arg Ala
53      55      60      65
55 gcc ctc cgc gcc ctt cgc ctg cgc tgc cgc acc cag tgt gcc gcc gac      297
56 Ala Leu Arg Ala Leu Arg Leu Arg Cys Arg Thr Gln Cys Ala Ala Asp
57      70      75      80
59 ttc ccg tgg gag ctg gac ccc gac tgg tcc ccc agc ccg gcc cag gcc      345
60 Phe Pro Trp Glu Leu Asp Pro Asp Trp Ser Pro Ser Pro Ala Gln Ala
61      85      90      95
63 tcg ggc gcc ggc gcc ctg cgc gac ctg agc ttc ttc ggg ggc ctt ctg      393

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64 Ser Gly Ala Gly Ala Leu Arg Asp Leu Ser Phe Phe Gly Gly Leu Leu
65      100                      105                      110
67 cgt cgc gct gcc tgc ctg cgc cgc tgc ctc ggg ccg ccg gcc gcc cac      441
68 Arg Arg Ala Ala Cys Leu Arg Arg Cys Leu Gly Pro Pro Ala Ala His
69 115                      120                      125                      130
71 tcg ctc agc gaa gag atg gag ctg gag ttc cgc aag cgg agc ccc tac      489
72 Ser Leu Ser Glu Glu Met Glu Leu Glu Phe Arg Lys Arg Ser Pro Tyr
73      135                      140                      145
75 aac tac ctg cag gtc gcc tac ttc aag atc aac aag ttg gag aaa gct      537
76 Asn Tyr Leu Gln Val Ala Tyr Phe Lys Ile Asn Lys Leu Glu Lys Ala
77      150                      155                      160
79 gtt gct gca gca cac acc ttc ttc gtg ggc aat cct gag cac atg gaa      585
80 Val Ala Ala Ala His Thr Phe Phe Val Gly Asn Pro Glu His Met Glu
81      165                      170                      175
83 atg cag cag aac cta gac tat tac caa acc atg tct gga gtg aag gag      633
84 Met Gln Gln Asn Leu Asp Tyr Tyr Gln Thr Met Ser Gly Val Lys Glu
85      180                      185                      190
87 gcc gac ttc aag gat ctt gag act caa ccc cat atg caa gaa ttt cga      681
88 Ala Asp Phe Lys Asp Leu Glu Thr Gln Pro His Met Gln Glu Phe Arg
89 195                      200                      205                      210
91 ctg gga gtg cga ctc tac tca gag gaa cag cca cag gaa gct gtg ccc      729
92 Leu Gly Val Arg Leu Tyr Ser Glu Glu Gln Pro Gln Glu Ala Val Pro
93      215                      220                      225
95 cac cta gag gcg gcg ctg caa gaa tac ttt gtg gcc tat gag gag tgc      777
96 His Leu Glu Ala Ala Leu Gln Glu Tyr Phe Val Ala Tyr Glu Glu Cys
97      230                      235                      240
99 cgt gcc ctc tgc gaa ggg ccc tat gac tac gat ggc tac aac tac ctt      825
100 Arg Ala Leu Cys Glu Gly Pro Tyr Asp Tyr Asp Gly Tyr Asn Tyr Leu
101      245                      250                      255
103 gag tac aac gct gac ctc ttc cag gcc atc aca gat cat tac atc cag      873
104 Glu Tyr Asn Ala Asp Leu Phe Gln Ala Ile Thr Asp His Tyr Ile Gln
105      260                      265                      270
107 gtc ctc aac tgt aag cag aac tgt gtc acg gag ctt gct tcc cac cca      921
108 Val Leu Asn Cys Lys Gln Asn Cys Val Thr Glu Leu Ala Ser His Pro
109 275                      280                      285                      290
111 agt cga gag aag ccc ttt gaa gac ttc ctc cca tcg cat tat aat tat      969
112 Ser Arg Glu Lys Pro Phe Glu Asp Phe Leu Pro Ser His Tyr Asn Tyr
113      295                      300                      305
115 ctg cag ttt gcc tac tat aac att ggg aat tat aca caa gct ggt gaa      1017
116 Leu Gln Phe Ala Tyr Tyr Asn Ile Gly Asn Tyr Thr Gln Ala Gly Glu
117      310                      315                      320
119 tgt gcc aag acc tat ctt ctc ttc ttc ccc aat gac gag gtg atg aac      1065
120 Cys Ala Lys Thr Tyr Leu Leu Phe Phe Pro Asn Asp Glu Val Met Asn
121      325                      330                      335
123 caa aat ttg gcc tat tat gca gct atg ctt gga gaa gaa cac acc aga      1113
124 Gln Asn Leu Ala Tyr Tyr Ala Ala Met Leu Gly Glu Glu His Thr Arg
125      340                      345                      350
127 tcc atc ggc ccc cgt gag cag ggc acc tagggaaaga tgtgaccccg      1160
128 Ser Ile Gly Pro Arg Glu Gln Gly Thr

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129 355          360
131 gaaagtactc agtttccctg ccctggagtg ccaaggagta ccgacagcga agcctactgg 1220
132 aaaaagaact gcttttcttc gcttatgatg tttttggaat tccctttgtg gatcgggatt 1280
133 catggactcc agaagaaatg attcccaaga aattgcaaga gaaacagaag tgaggacctt 1340
134 gaagaaactg catggttgga tcagtctgat gaagcacttg aggcttcttg agcccaggca 1400
135 gatgtgaact cctggcaagg ggtgggcagg tccagtttgg gaagtcgggg tggagcccag 1460
136 ggctggccct ggaatgcagt cctcagagcg gttgtgctca taggtcagaa cgggaaacag 1520
137 ccgtacgcat ctcccaggag attgggaacc ttatgaagga aatcgagacc ctgtgtggaag 1580
138 agaagaccaa ggagtcactg gatgtgagca gactgacctg ggaagggtggc cccctgctgt 1640
139 atgaaggcat cagtctcacc atgaactcca aactcctgaa tggttaccag cgggtgtgta 1700
140 tggacggcgt aatctctgac cagcagtgctc aggagctgca gagactgacc aatgtggcag 1760
141 caacctcagg agatggctac cggggtcaga cctcccaca tactcccaat gaaaagtctt 1820
142 atggtgtcac tgtcttcaaa gccctcaagc tggggcaaga aggcaaagtt cctctgcaga 1880
143 gtgcccacct gtactacaac gtgacggaga aagtgcggcg catcatggag tcctacttcc 1940
144 gcctggatac gccctcttac ttttcctact ctcatctggt gtgccgcaact gccatcgaag 2000
145 aggtccaggc agagaggaag gatgatagtc atccagtcca cgtggacaac tgcacctga 2060
146 atgccgagac cctcgtgtgt gtcaaagagc cccagccta caccttcgcg gactacagcg 2120
147 ccacctctta cctaaatggg gacttcgatg gcggaaactt ttatttcact gaactggatg 2180
148 ccaagaccgt gacggcagag gtgcagcctc agtgtggaag agccgtggga ttctcttcag 2240
149 gcaactgaaa cccacatgga gtgaaggctg tcaccagggg gcagcgctgt gccatcgccc 2300
150 tgtggttcac cctggacctt cgacacagcg agcgggacag ggtgcaggca gatgacctgg 2360
151 tgaagatgct cttcagccca gaagagatgg acctctccca ggagcagccc ctggatgccc 2420
152 agcaggggcc ccccgaaact gcacaagagt ctctctcagg cagtgaatcg aagcccaagg 2480
153 atgagctatg acagcgtcca ggtcagacgg atgggtgact agacccatga agaggaactc 2540
154 ttcttgcaact ctgagctggc cagcccctcg gggctgcaga gcagtgaacc tacatctgcc 2600
155 actcagccga ggggacctg ctacacagct tctacatggt gctactgctc ttggagtggg 2660
156 catgaccaga caccgcaccc cctggatctg gctgagggtc caggacacag gccagccac 2720
157 cccagggggc ctccacaggc cgctgcataa cagcgataca gtacttaagt gtctgtgtag 2780
158 acaaccaaag aataaatgat tcatggtttt ttttaaaaaa aaaaaaaaaa 2829
160 <210> SEQ ID NO: 2
161 <211> LENGTH: 363
162 <212> TYPE: PRT
163 <213> ORGANISM: Homo sapiens
165 <400> SEQUENCE: 2
166 Met Ala Val Arg Ala Leu Lys Leu Leu Thr Thr Leu Leu Ala Val Val
167 1 5 10 15
168 Ala Ala Ala Ser Gln Ala Glu Val Glu Ser Glu Ala Gly Trp Gly Met
169 20 25 30
170 Val Thr Pro Asp Leu Leu Phe Ala Glu Gly Thr Ala Ala Tyr Ala Arg
171 35 40 45
172 Gly Asp Trp Pro Gly Val Val Leu Ser Met Glu Arg Ala Leu Arg Ser
173 50 55 60
174 Arg Ala Ala Leu Arg Ala Leu Arg Leu Arg Cys Arg Thr Gln Cys Ala
175 65 70 75 80
176 Ala Asp Phe Pro Trp Glu Leu Asp Pro Asp Trp Ser Pro Ser Pro Ala
177 85 90 95
178 Gln Ala Ser Gly Ala Gly Ala Leu Arg Asp Leu Ser Phe Phe Gly Gly
179 100 105 110
180 Leu Leu Arg Arg Ala Ala Cys Leu Arg Arg Cys Leu Gly Pro Pro Ala

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181          115          120          125
182 Ala His Ser Leu Ser Glu Glu Met Glu Leu Glu Phe Arg Lys Arg Ser
183          130          135          140
184 Pro Tyr Asn Tyr Leu Gln Val Ala Tyr Phe Lys Ile Asn Lys Leu Glu
185 145          150          155          160
186 Lys Ala Val Ala Ala His Thr Phe Phe Val Gly Asn Pro Glu His
187          165          170          175
188 Met Glu Met Gln Gln Asn Leu Asp Tyr Tyr Gln Thr Met Ser Gly Val
189          180          185          190
190 Lys Glu Ala Asp Phe Lys Asp Leu Glu Thr Gln Pro His Met Gln Glu
191          195          200          205
192 Phe Arg Leu Gly Val Arg Leu Tyr Ser Glu Glu Gln Pro Gln Glu Ala
193          210          215          220
194 Val Pro His Leu Glu Ala Ala Leu Gln Glu Tyr Phe Val Ala Tyr Glu
195 225          230          235          240
196 Glu Cys Arg Ala Leu Cys Glu Gly Pro Tyr Asp Tyr Asp Gly Tyr Asn
197          245          250          255
198 Tyr Leu Glu Tyr Asn Ala Asp Leu Phe Gln Ala Ile Thr Asp His Tyr
199          260          265          270
200 Ile Gln Val Leu Asn Cys Lys Gln Asn Cys Val Thr Glu Leu Ala Ser
201          275          280          285
202 His Pro Ser Arg Glu Lys Pro Phe Glu Asp Phe Leu Pro Ser His Tyr
203          290          295          300
204 Asn Tyr Leu Gln Phe Ala Tyr Tyr Asn Ile Gly Asn Tyr Thr Gln Ala
205 305          310          315          320
206 Gly Glu Cys Ala Lys Thr Tyr Leu Leu Phe Phe Pro Asn Asp Glu Val
207          325          330          335
208 Met Asn Gln Asn Leu Ala Tyr Tyr Ala Ala Met Leu Gly Glu Glu His
209          340          345          350
210 Thr Arg Ser Ile Gly Pro Arg Glu Gln Gly Thr
211          355          360
213 <210> SEQ ID NO: 3
214 <211> LENGTH: 2600
215 <212> TYPE: DNA
216 <213> ORGANISM: Homo sapiens
218 <220> FEATURE:
219 <221> NAME/KEY: CDS
220 <222> LOCATION: (52)...(2259)
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224                                     Met Ala
225                                     1
227 gta cgc gcg ttg aag ctg ctg acc aca ctg ctg gct gtc gtg gcc gct      105
228 Val Arg Ala Leu Lys Leu Leu Thr Thr Leu Leu Ala Val Val Ala Ala
229          5          10          15
231 gcc tcc caa gcc gag gtc gag tcc gag gca gga tgg ggc atg gtg acg      153
232 Ala Ser Gln Ala Glu Val Glu Ser Glu Ala Gly Trp Gly Met Val Thr
233          20          25          30
235 cct gat ctg ctc ttc gcc gag ggg acc gca gcc tac gcg cgc ggg gac      201

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236 Pro Asp Leu Leu Phe Ala Glu Gly Thr Ala Ala Tyr Ala Arg Gly Asp
237 35 40 45 50
239 tgg ccc ggg gtg gtc ctg agc atg gaa cgg gcg ctg cgc tcc cgg gca 249
240 Trp Pro Gly Val Val Leu Ser Met Glu Arg Ala Leu Arg Ser Arg Ala
241 55 60 65
243 gcc ctc cgc gcc ctt cgc ctg cgc tgc cgc acc cag tgt gcc gcc gac 297
244 Ala Leu Arg Ala Leu Arg Leu Arg Cys Arg Thr Gln Cys Ala Ala Asp
245 70 75 80
247 ttc ccg tgg gag ctg gac ccc gac tgg tcc ccc agc ccg gcc cag gcc 345
248 Phe Pro Trp Glu Leu Asp Pro Asp Trp Ser Pro Ser Pro Ala Gln Ala
249 85 90 95
251 tcg ggc gcc ggc gcc ctg cgc gac ctg agc ttc ttc ggg ggc ctt ctg 393
252 Ser Gly Ala Gly Ala Leu Arg Asp Leu Ser Phe Phe Gly Gly Leu Leu
253 100 105 110
255 cgt cgc gct gcc tgc ctg cgc cgc tgc ctc ggg ccg ccg gcc gcc cac 441
256 Arg Arg Ala Ala Cys Leu Arg Arg Cys Leu Gly Pro Pro Ala Ala His
257 115 120 125 130
259 tcg ctc agc gaa gag atg gag ctg gag ttc cgc aag ccg agc ccc tac 489
260 Ser Leu Ser Glu Glu Met Glu Leu Glu Phe Arg Lys Arg Ser Pro Tyr
261 135 140 145
263 aac tac ctg cag gtc gcc tac ttc aag atc aac aag ttg gag aaa gct 537
264 Asn Tyr Leu Gln Val Ala Tyr Phe Lys Ile Asn Lys Leu Glu Lys Ala
265 150 155 160
267 gtt gct gca gca cac acc ttc ttc gtg ggc aat cct gag cac atg gaa 585
268 Val Ala Ala Ala His Thr Phe Phe Val Gly Asn Pro Glu His Met Glu
269 165 170 175
271 atg cag cag aac cta gac tat tac caa acc atg tct gga gtg aag gag 633
272 Met Gln Gln Asn Leu Asp Tyr Tyr Gln Thr Met Ser Gly Val Lys Glu
273 180 185 190
275 gcc gac ttc aag gat ctt gag act caa ccc cat atg caa gaa ttt cga 681
276 Ala Asp Phe Lys Asp Leu Glu Thr Gln Pro His Met Gln Glu Phe Arg
277 195 200 205 210
279 ctg gga gtg cga ctc tac tca gag gaa cag cca cag gaa gct gtg ccc 729
280 Leu Gly Val Arg Leu Tyr Ser Glu Glu Gln Pro Gln Glu Ala Val Pro
281 215 220 225
283 cac cta gag gcg gcg ctg caa gaa tac ttt gtg gcc tat gag gag tgc 777
284 His Leu Glu Ala Ala Leu Gln Glu Tyr Phe Val Ala Tyr Glu Glu Cys
285 230 235 240
287 cgt gcc ctc tgc gaa ggg ccc tat gac tac gat ggc tac aac tac ctt 825
288 Arg Ala Leu Cys Glu Gly Pro Tyr Asp Tyr Asp Gly Tyr Asn Tyr Leu
289 245 250 255
291 gag tac aac gct gac ctc ttc cag gcc atc aca gat cat tac atc cag 873
292 Glu Tyr Asn Ala Asp Leu Phe Gln Ala Ile Thr Asp His Tyr Ile Gln
293 260 265 270
295 gtc ctc aac tgt aag cag aac tgt gtc acg gag ctt gct tcc cac cca 921
296 Val Leu Asn Cys Lys Gln Asn Cys Val Thr Glu Leu Ala Ser His Pro
297 275 280 285 290
299 agt cga gag aag ccc ttt gaa gac ttc ctc cca tcg cat tat aat tat 969
300 Ser Arg Glu Lys Pro Phe Glu Asp Phe Leu Pro Ser His Tyr Asn Tyr

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 2376
Seq#:7; N Pos. 2282

VERIFICATION SUMMARY

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Input Set : A:\06501-091001.TXT

Output Set: N:\CRF3\05022002\J045815.raw

L:530 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:721 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:2372
L:837 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:987 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:2227